

Supplemental File 2. Mass Spectrometry Data. The following information is given to highlight the MS/MS spectra for the 8 proteins identified with a single peptide showed in Tables 2 and 4.

Precursor 1348.667Da MS/MS results (protein ID 294 - putative HSP90lamine A/C)

Mascot Search Results

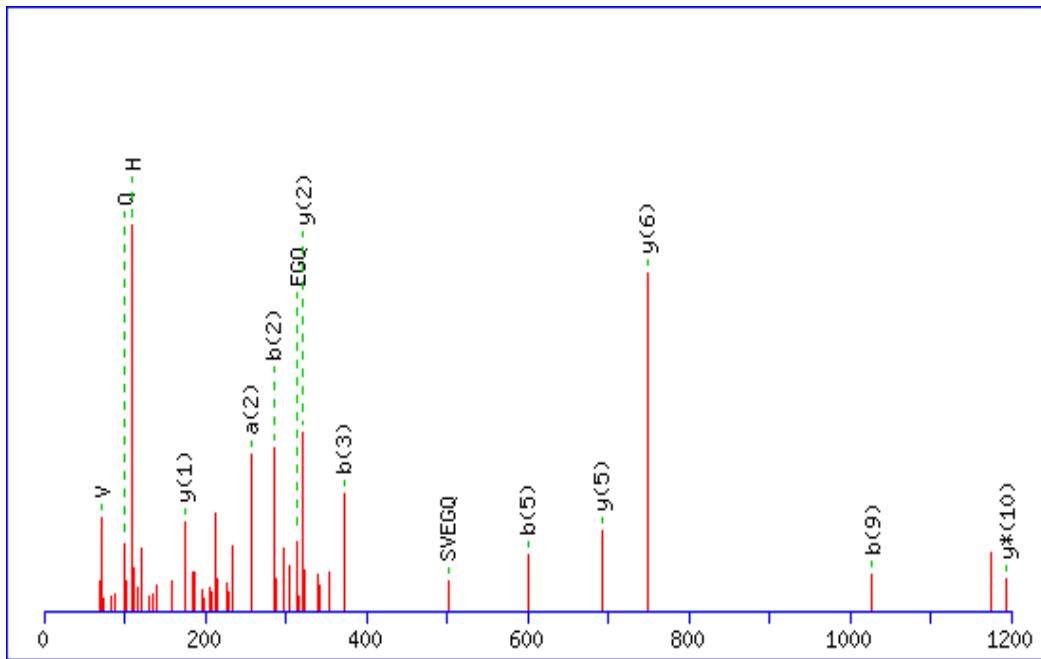
Match to: H90B3_HUMAN Score: 40
Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1

1 MPEEVHHGEE EVETFAFQAE IAQLISLIIN TFYSNEEIFL QELISNASDA
51 LDKIRYESLT DPSKLD SGKE LKIDIIPNPQ ERTLALVDTG
IGMTKADLIN
101 NLRTIAKSGT KACMEALQAE KLVVITKHND DEQYAWESSA
GGSFTVHADH
151 GEPIGRGTKV ILHLKEDQTE YLEERRVKEV VKKHSQFIGY PITLYLEKEQ
201 DKEISDDEAE EEKGEKEEED KDDEEKPKIK DVGSDEEDDS KEYGEFYKSL
251 TSDWEDHLAV **KHFSVEGQLE** FRALLFSPRR APFDLFENKK KKNNIKLYVR
301 RVFIMDSCDE LIPEYLNFIH GVVDSEDLPL NISREMLQQS KILKYVSHMK
351 ETQKSTYYIT GESKEQVANS AFVERVRKQG FEVVYMTEPI
DEYCVQQLKE
401 FDGKSLSVST KEGLELPEDE EEKKKMEESK EKFNELCKLM KEILDKKVEK
451 VTISNRLVSS PCCIVTSTYG WTANMEQIMK AQALRDNSTM
GYMMAKKHLE
501 INPDHPIMET LRQKAEADKN DKAVKDLVVL LFETALLSSG FSLEDPQTHS
551 NHIYHMIKLG LGTDEDEVAA EEPSDAVPDE IPPLEGDEDA
SRMEEVD

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
262 - 272	1348.667	1347.659	1347.657	2	0	K.HFSVEGQLEFR.A

(Ions score 40)

MS/MS Fragmentation of **KHFSVEGQLEFR**
Found in **H90B3_HUMAN**, Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens
GN=HSP90AB3P PE=5 SV=1



#	b	Seq.	y	#
1	138.066	H		11
2	285.135	F	1211.606	10
3	372.167	S	1064.537	9
4	471.235	V	977.505	8
5	600.278	E	878.437	7
6	657.299	G	749.394	6
7	785.358	Q	692.373	5
8	898.442	L	564.314	4
9	1027.484	E	451.23	3
10	1174.553	F	322.187	2
11		R	175.119	1

Precursor 1023.503Da MS/MS results (protein ID 580 - Lamine A/C)

Mascot Search Results

Match to: LMNA_HUMAN Score: 38 Expect: 3.6

Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1

1 METPSQRRAT RSGAQASSTP LSPTRITRLQ EKEDLQELND

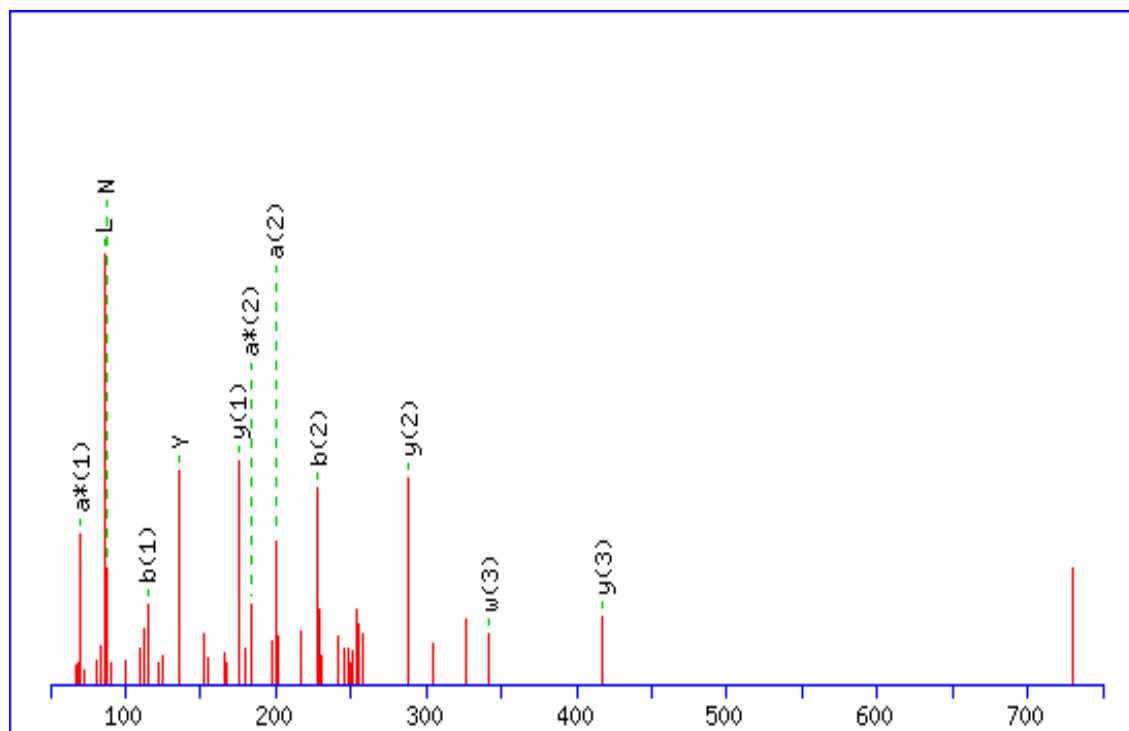
RLAVYIDRVR

51 SLETENAGLR LRITSEEEVV SREVSGIKAA YEAELGDARK TLDSVAKERA

101 RLQLELSKVR EEFKELKARN TKKEGDLIAA QARLKDLEAL LNSKEAALST
 151 ALSEKRTLEG ELHDLRGQVA KLEAALGEAK KQLQDEMLRR
 VDAENRLQTM
 201 KEELDFQK**NI YSEEL**RETKR RHETRLVEID NGKQREFESR LADALQELRA
 251 QHEDQVEQYK KELEKTYSAK LDNARQSAER NSNLVGAAHE
 ELQQSRIRID
 301 SLQAQLSQLQ KQLAAKEAKL RDLEDLARE RDTSRRLAE
 KEREMAEMRA
 351 RMQQQLDEYQ ELLDIKLALD MEIHAYRKLL EGEEERLRLS PSPTSQRSRG
 401 RASSHSSQTQ GGGSVTKKRK LESTESRSSF SQHARTSGRV
 AVEEVDEEGK
 451 FVRLRNKSNE DQSMGNWQIK RQNGDDPLL T YRFPKFTLK
 AGQVVTIWA
 501 GAGATHSPPT DLVWKAQNTW GCGNSLRTAL INSTGEEVAM
 RKLVRSVTVV
 551 EDDDEDGDD LLHHHHGSHC SSSGDPAEYN LRSRTVLCGT
 CGQPADKASA
 601 SGGAQVGGP ISSGSSASSV TVTRSYRSVG GSGGGSFGDN
 LVTRSYLLGN
 651 SSPRTQSPQN CSIM

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
209 - 216	1023.503	1022.496	1022.503	-7	0	K.NIYSEELR.E (Ions score 24)

MS/MS Fragmentation of **NIYSEELR**
 Found in **LMNA_HUMAN**, Lamin-A/C OS=Homo sapiens GN=LMNA PE=1
 SV=1



#	b	Seq.	y	#
1	115.05	N		8
2	228.134	I	909.468	7
3	391.198	Y	796.384	6
4	478.23	S	633.32	5
5	607.272	E	546.288	4
6	736.315	E	417.246	3
7	849.399	L	288.203	2
8		R	175.119	1

Precursor 1023.503Da MS/MS results (protein ID 580 - coatamer subunit-alpha)

Mascot Search Results

Match to: COPA_HUMAN Score: 37

Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2

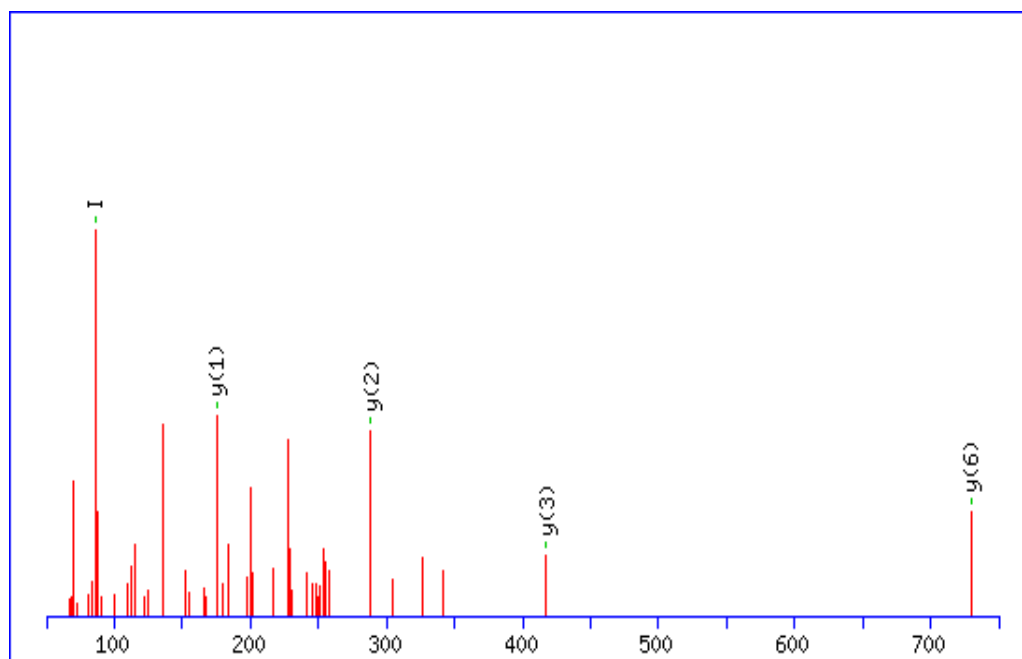
1 MLTKFETKSA RVKGLSFHPK RPWILTSLHN GVIQLWDYRM
CTLIDKFDEH
51 DGPVRGIDFH KQQPLFVSGG DDYKIKVWNY KLRRCLFTLL GHLDYIRTTF
101 FHHEYPPWILS ASDDQTIRVW NWQSRTCVCV LTGHNHYVMC
AQFHPTEDLV
151 VSASLDQTVR VWDISGLRKK NLSPGAVESD VRGITGVDLF GTTDAVVKHV
201 LEGHDRGVNW AAFHPTMPLI VSGADDRQVK IWRMNESKAW
EVDTCRGHYN
251 NVSCAVFHPR QELILSNSED KSIRVWDMSK RTGVQTFRRD
HDRFWVLAHH
301 PNLNLFAAGH DGGMIVFKLE RERPAYAVHG NMLHYVKDRF
LRQLDFNSSK
351 DVAVMQLRSG SKFPVFNMSY NPAENAVLLC TRASNLNST YDLYTIPKDA
401 DSQNPDAPEG KRSSGLTAVW VARNRFAVLD RMHSLLIKNL
KNEITKKVQV
451 PNCDEIFYAG TGNLLLRDAD SITLFDVQQK RTLASVKISK VKYVIWSADM
501 SHVALLAKHA IVICNRKLDA LCNIHENIRV KSGAWDESGV
FIYTTSNHIK
551 YAVTTGDHGI IRTLDLPIYV TRVKGNNVYC LDRECRPRVL TIDPTEFKFK
601 LALINRKYDE VLHMVRNAKL VGQSIIAYLQ KKGYPEVALH FVKDEKTRFS
651 LALECGNIEI ALEAAKALDD KNCWEKLGEV ALLQGNHQIV EMCYQRTKNF
701 DKLSFLYLIT GNLEKLRKMM KIAEIRKDMS GHYQNALYLG DVSERVRILK
751 NCGQKSLAYL TAATHGLDEE AESLKETFDP EKETIPDIDP NAKLLQPPAP
801 IMPLDTNWPL LTVSKGFFEG TIASKGKGGA LAADIDIDTV GTEGWGEDAE

851 LQLDEDFVE ATEGLGDDAL GKGQEEGGGW DVEEDLELPP
 ELDISPGAAG
 901 GAEDGFFVPP TKGTSPTQIW CNNSQLPVDH ILAGSFETAM RLLHDQVGVI
 951 QFGPYKQLFL QTYARGRTTY QALPCLPSMY GYPNRNWKDA
 GLKNGVPAVG
 1001 LKLNDLIQRL QLCYQLTTVG KFEEAVEKFR SILLSVPLL VDNKQEIAEA
 1051 QQLITICREY IVGLSVETER KKLPKETLEQ QKRICEMAAY FTHTSNLQPVH
 1101 MILVLR TALN LFFKLKNFKT AATFARRLLE LGPKPEVAQQ TRKILSACEK
 1151 NPTDAYQLNY DMHNPF DICA ASYRPIYRGK PVEKCPLSGA
 CYSPEFKGQI
 1201 CRVTTVTEIG KDVIGLRISP LQFR

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
719 - 726	1023.503	1022.496	1022.525	-29	1	K.MMKIAEIR.K 2 __Oxidation (M) (Ions score 37)

MS/MS Fragmentation of **MMKIAEIR**

Found in **COPA_HUMAN**, Coatomer subunit alpha OS=Homo sapiens GN=COPA
 PE=1 SV=2



#	b	Seq.	y	#
1	84.044	M		8
2	167.082	M	812.499	7
3	295.176	K	729.462	6
4	408.261	I	601.367	5
5	479.298	A	488.283	4
6	608.34	E	417.246	3
7	721.424	I	288.203	2
8		R	175.119	1

Precursor 1370.688Da MS/MS results (protein ID 598 - UDP glucose 6 deshydrogenase)

Mascot Search Results

Match to: UGDH_HUMAN Score: 39

UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1

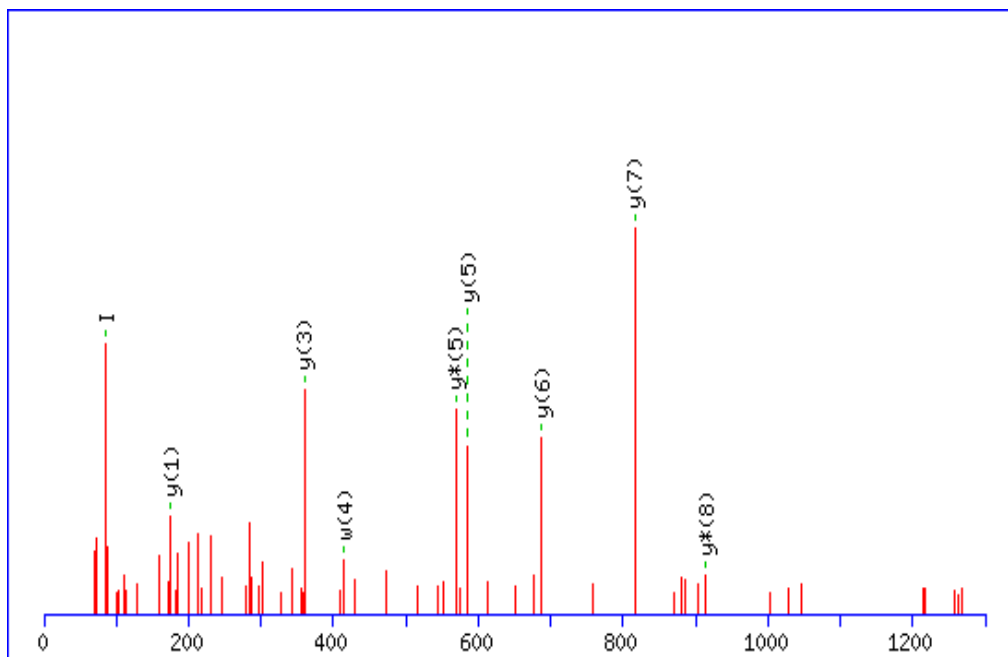
Matched peptides shown in **Bold Red**

1 MFEIKKICCI GAGYVGGPTC SVIAHMCPEI RVTVVDVNES
RINAWNSPTL
51 PIYEPGLKEV VESCRGKNLF FSTNIDDAIK EADLVFISVN TPTKTYGMGK
101 GRAADLKYIE ACARRIVQNS NGYKIVTEKS TVPVRAAESI RRIFDANTKP
151 NLNLQVLSNP EFLAEGTAIK DLKNPDR**VLI GGDETPEGQR** AVQALCAVYE
201 HWVPREKILT TNTWSSELSK LAANAFLAQR ISSINSISAL CEATGADVEE
251 VATAIGMDQR IGNKFLKASV GFGGSCFQKD VLNLVYLCEA
LNLPEVARYW
301 QQVIDMNDYQ RRRFASRIID SLFNTVTDKK IAILGFAFKK DTGDTRESSS
351 IYISKYLMDE GAHLHIYDPK VPREQIVVDL SHPGVSEDDQ VSRLVTISKD
401 PYEACDGAHA VVICTEWD MF KELDYERIEH KMLKPAFIFD GRRVLDGLHN
451 ELQTIGFQIE TIGKKVSSKR IPYAPSGEIP KFSLQDPPNK KPKV

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
178 - 190	1370.688	1369.681	1369.684	-2	0	R.VLIGDETPEGQR.A (Ions score 39)

MS/MS Fragmentation of **VLIGDETPEGQR**

Found in **UGDH_HUMAN**, UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1



#	b	Seq.	y	#
1	100.076	V		13
2	213.16	L	1271.623	12
3	326.244	I	1158.539	11
4	383.265	G	1045.454	10
5	440.287	G	988.433	9
6	555.314	D	931.412	8
7	684.356	E	816.385	7
8	785.404	T	687.342	6
9	882.457	P	586.294	5
10	1011.499	E	489.242	4
11	1068.521	G	360.199	3
12	1196.579	Q	303.178	2
13		R	175.119	1

Precursor 1214.597Da MS/MS results (protein ID 953 - fumarate hydratase mitochondriale)

Mascot Search Results

Match to: FUMH_HUMAN Score: 61

Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3

Matched peptides shown in **Bold Red**

1 MYRALRLLAR SRPLVRAPAA ALASAPGLGG AAVPSFWPPN

AARMASQNSF

51 RIEYDTFGEL KVPNDKYYGA QTVRSTMNFK IGGVTERMPT PVIKAFGILK

101 RAAAEVNQDY GLDPKIANAI MKAADVAEG KLNDHFPLVV

WQTGSGTQTN

151 MNVNEVISNR AIEMLGELG SKIPVHPNDH VNKSQSSNDT FPTAMHIAAA

201 IEVHEVLLPG LQKLHDALDA KSKEFAQIIK IGRHTHTQDAV PLTLGQEFSG

251 YVQQVKYAMT RIKAAAMPRIY ELAAGGTAVG TGLNTRIGFA EKVAAKVAAL

301 TGLPFVTAPN KFEALAAHDA LVELSGAMNT TACSLMKIAN DIRFLGSGPR

351 SGLGELILPE NEPGSSIMPG KVNPTQCEAM TMVAAQVMGN

HVAVTVGGSN

401 GHFELNVFKP MMIKNVLHSA RLLGDASVSF TENCVVGIQA NTERINKLMN

451 ESLMLVTALN PHIGYDKA AK IAKTAHKNGS TLKETAIELG YLTAEQFDEW

501 VKPKDMLGPK

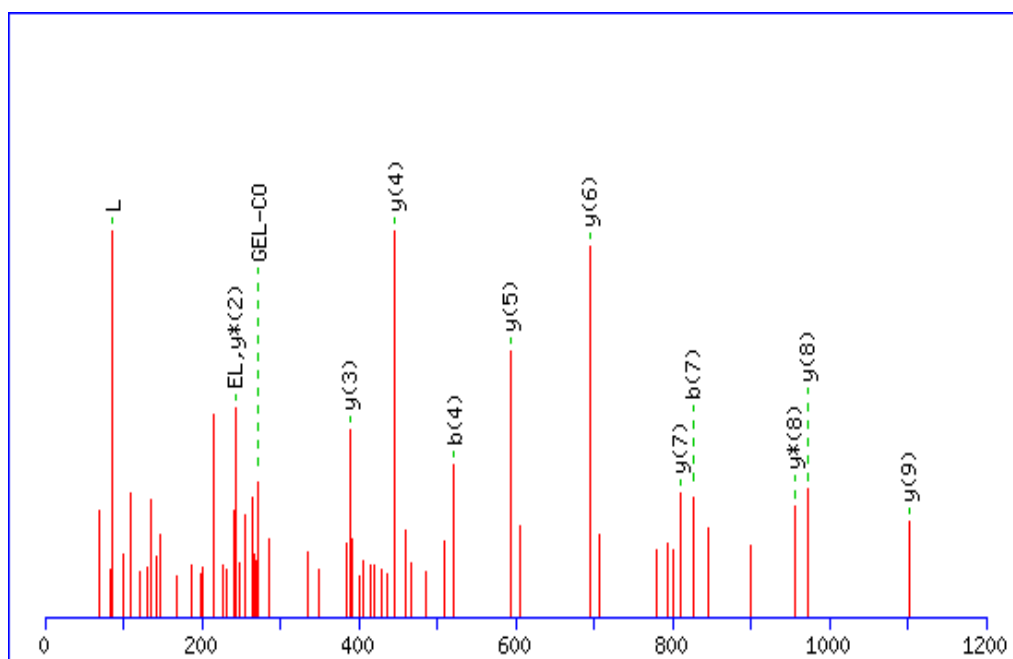
Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
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52 - 61	1214.597	1213.590	1213.587	3	0	R.IEYDTFGELK.V
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(Ions score 61)

MS/MS Fragmentation of **IEYDTFGELK**

Found in **FUMH_HUMAN**, Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FUH
PE=1 SV=3



#	b	Seq.	y	#
1	114.091	I		10
2	243.134	E	1101.51	9
3	406.197	Y	972.467	8
4	521.224	D	809.404	7
5	622.272	T	694.377	6
6	769.34	F	593.329	5
7	826.362	G	446.261	4
8	955.404	E	389.239	3
9	1068.488	L	260.197	2
10		K	147.113	1

Precursor 927.552Da MS/MS results (protein ID 1821 - Fatty acid-binding protein, epidermal)

Mascot Search Results

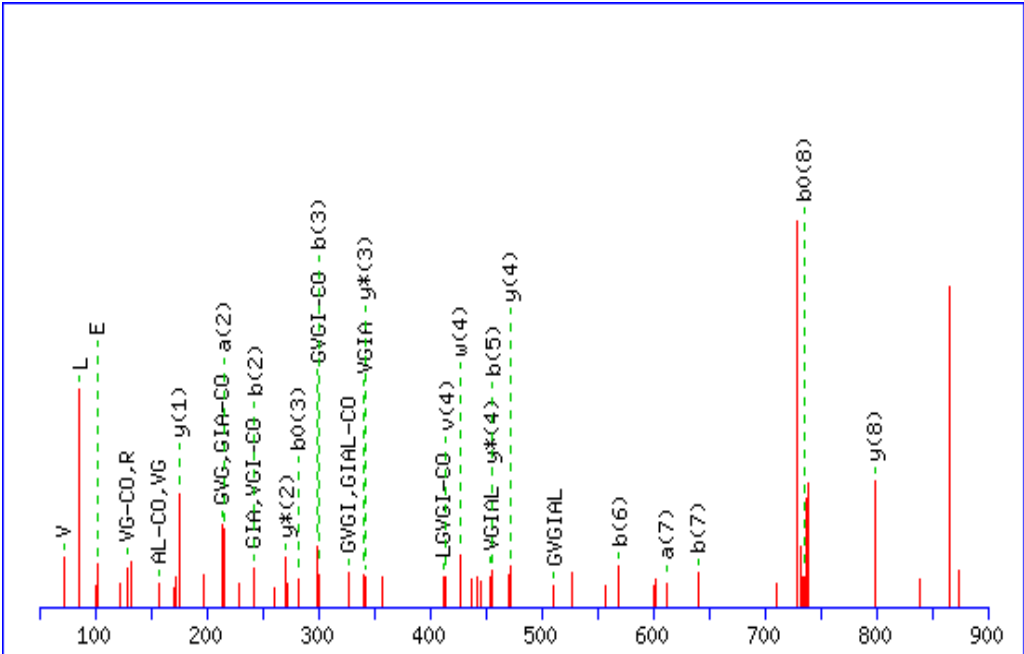
Match to: FABP5_HUMAN Score: 26

Fatty acid-binding protein, epidermal - Homo sapiens (Human)

Matched peptides shown in **Bold Red**

1 MATVQQLEGR WRLVDSKGFDEYMK**ELGVGI ALR**KMGAMAK PDCIITCDGK
51 NLTIKTESTL KTTQFSCTLG EKFEETTADG RKTQTVCNFT DGALVQHQEW
101 DGKESTITRK LKDGKLVVEC VMNNVTCTRI YEKVE

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
25 - 33	927.552	926.545	926.555	-11	0	K.ELGVGIALR.K (Ions score 26)



#	b	Seq.	y	#
1	130.05	E		9
2	243.134	L	798.52	8
3	300.155	G	685.436	7
4	399.224	V	628.414	6
5	456.245	G	529.346	5
6	569.329	I	472.324	4
7	640.366	A	359.24	3
8	753.451	L	288.203	2
9		R	175.119	1

Precursor 1388.841Da MS/MS results (protein ID 2120 - Poly(rC)-binding protein 1)

Mascot Search Results

Match to: PCBP1_HUMAN Score: 36

Poly(rC)-binding protein 1 - Homo sapiens (Human)

1 MDAGVTESGL NVTLTIRLLM HGKEVGSIIG KKGESVKRIR

EESGARINIS

51 EGNCPER IIT LTGPTNAIFK AFAMIIDKLE EDINSSMTNS TAASRPPVTL

101 RLVPATQCG SLIGKGGCKI KEIRESTGAQ VQVAGDMLPN STERAITAG

151 VPQSVTECVK QICLVMLETL SQSPQGRVMT IPYQPMPASS

PVICAGGQDR

201 CSDAAGYPHA THDLEGPLD AYSIQGQHTI SPLDLAKLNQ

VARQQSHFAM

251 MHGGTGFAGI DSSSPEVKGY WASLDASTQT THELTIPNNL IGCIIQRQGA

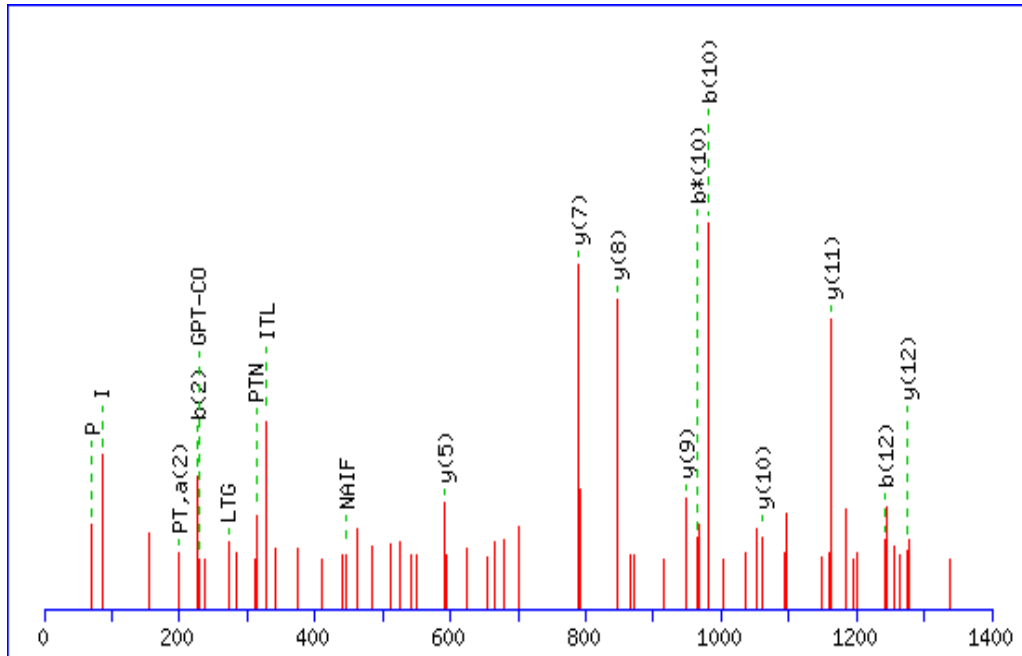
301 NINEIRQMSG AQIKIANPVE GSSGRQVTIT GSAASISLAQ

YLINARLSSE

351 KGMGCS

Start - End Observed Mr(expt) Mr(calc) ppm Miss Sequence

58 - 70 1388.841 1387.833 1387.807 19 0 R.IITLTGPTNAIFK.A
(Ions score 36)



#	b	Seq.	y	#
1	114.091	I		13
2	227.175	I	1275.731	12
3	328.223	T	1162.647	11
4	441.307	L	1061.599	10
5	542.355	T	948.515	9
6	599.376	G	847.467	8
7	696.429	P	790.446	7
8	797.477	T	693.393	6
9	911.52	N	592.345	5
10	982.557	A	478.302	4
11	1095.641	I	407.265	3
12	1242.709	F	294.181	2
13		K	147.113	1

Precursor 914.507Da MS/MS results (protein ID 2120 - Heterogeneous nuclear ribonucleoprotein D0)

Mascot Search Results

Match to: HNRPD_HUMAN Score: 44 Expect:

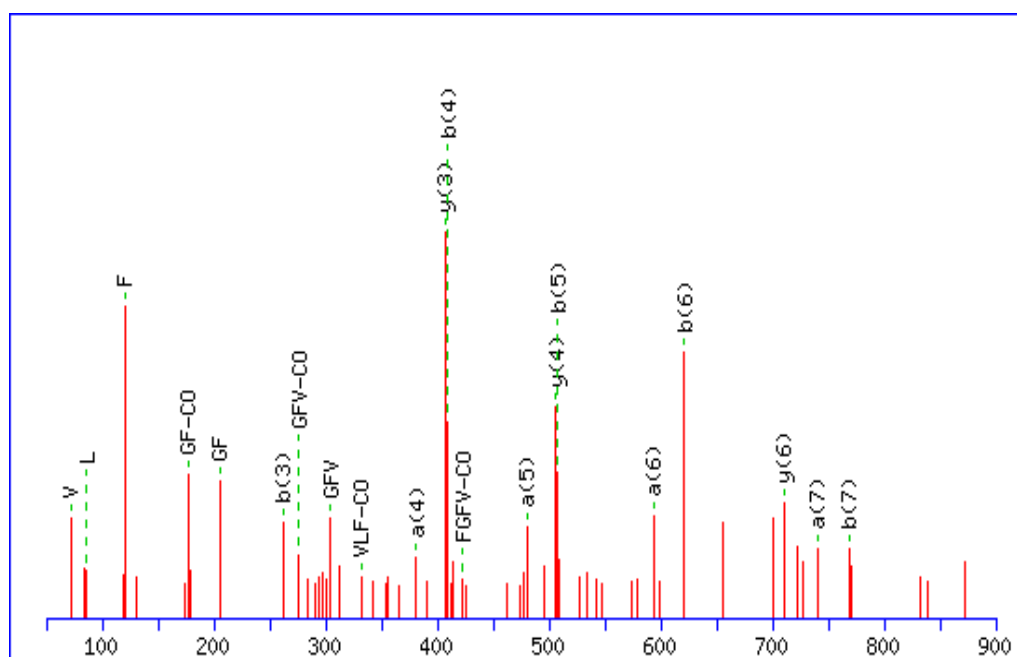
0.77

Heterogeneous nuclear ribonucleoprotein D0 - Homo sapiens (Human)

Matched peptides shown in **Bold Red**

1 MEVPPRLSHV PPPLFPSAPA TLASRSLSHW RPRPPRQLAP LLPSLAPSSA
51 RQGARRAQRH VTAQQPSRLA GGAAIKGGRR RRPDLFRRHF
KSSSIQRSAA
101 AAAATR TARQ HPPADSSVTM EDMNEYSNIE EFAEGSKINA
SKNQDDGKM
151 FIGGLSWDTS KDLTEYLSR FGEVVDCTIK TDPVTGRSR**G FGFVLFK**DAA
201 SVDKVLELKE HKLDGKLIDP KRAKALKGKE PPKKVFGVGL SPDTSEEQIK
251 EYFGAFGEIE NIELPMDTKT NERRGFCFIT YTDEEPVKKL LESRYHQIGS
301 GKCEIKVAQP KEVYRQQQQQ QKGGRGAAAG GRGGTRGRGR
GQQQNWNQGF
351 NNYYDQGYGN YNSAYGGDQN YSGYGGYDYT GYNYGN YGYG
QGYADYSGQQ
401 STYGKASRGG GNHQNNYPY

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
190 - 197	914.507	913.500	913.506	-7	0	R.GFGFVLFK.D (ions score 36)



#	b	Seq.	y	#
1	58.029	G		8
2	205.097	F	857.492	7
3	262.119	G	710.424	6
4	409.187	F	653.402	5
5	508.255	V	506.334	4
6	621.34	L	407.265	3
7	768.408	F	294.181	2
8		K	147.113	1